

REMARKS

Claims 1-2, 6-14, 16 and 28-33 are pending, upon entry of the amendment submitted above. Favorable reconsideration is respectfully requested.

Applicants would like to thank Examiner Fronda for the helpful and courteous discussion held with their representative on January 18, 2005 and a subsequent telephone discussion. During the discussions, the amendments presented above were discussed. Applicants' representative also presented the Examiner with the results of the BLASTN search attached hereto. As noted on the Interview Summary form, the "BLASTN search results-shows significant alignments to coryneform bacterium citrate synthases."

At the discussion, the Examiner indicated that the amendments appear to place the application in condition for allowance, and that a final decision would be made after a written response was filed. The following remarks expand on the discussion with the Examiner.

The rejection under 35 U.S.C. §112, first paragraph, is believed to be obviated by the amendments submitted above.

Claim 1 has been amended to specify a citrate synthase gene obtained from *Corynebacterium glutamicum* or *Brevibacterium lactofermentum*. Claim 16 has been amended to specify that the citrate synthase gene is obtained from corynebacterium chromosomal DNA by the polymerase chain reaction using oligonucleotide primers of SEQ ID NO: 1 and SEQ ID NO: 2.

In view of those amendments, the results of the BLASTN search enclosed herewith and the disclosure of Eikmanns et al., Applicants had possession of the claimed subject at the time the present application was filed. Accordingly, the written description requirement is satisfied, and withdrawal of this ground of rejection is respectfully requested.

Application No. 09/419,611
Reply to Office Action of August 25, 2004

The rejection under 35 U.S.C. §112, second paragraph, is respectfully traversed.

Claim 11 has been amended to specify that the citrate synthase gene is obtainable by PCR amplification of chromosomal DNA using primers of SEQ ID NO: 1 and SEQ ID NO:

2. Claims 15 and 17 have been cancelled.

In view of the foregoing, the claims are definite within the meaning of 35 U.S.C. §112, second paragraph. Accordingly, withdrawal of this ground of rejection is respectfully requested.

Applicants submit that the present application is in condition for allowance. Early notice to this effect is earnestly solicited.

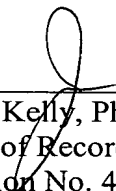
Respectfully submitted,

OBLON, SPIVAK, McCLELLAND,
MAIER & NEUSTADT, P.C.
Norman F. Oblon

Customer Number

22850

Tel: (703) 413-3000
Fax: (703) 413 -2220
(OSMMN 06/04)



James J. Kelly, Ph.D.
Attorney of Record
Registration No. 41,504

BLASTN Search Result

Computed at GenomeNet BLAST2 Server (Kyoto Center) on Thu Jan 6 11:07:20 JST 2005

Database Name NR-NT

>query

```
atgtttgaaa gggatatcgt ggctactgat aacaacaagg ctgtcctgca
ctaccccggt 60ggcgagtt cgaaatggac atcatcgagg cttctgaggg
taacaacggt gttgtcctgg gc120aagat gctgtctgag actggactga
tcacttttga cccaggttat gtgagcactg gctcc180ac cgagtccaag
atcacctaca tcgatggcga tgcgggaatc ctgcgttacc gcggctat24
0gacatcgct gatctggctg agaatgccac cttcaacgag gtttcttacc
tacttatcaa c300ggtgaa ctaccaaccc cagatgagct tcacaagttt
aacgacgaga ttgccacca cacc360ctt ctggacgagg acttcaagtc
ccagttcaac gtgttccac gcgacgctca cccaatg420 gcaaccttgg
cttcctcggt taacattttg tctacctact accaggatca gctgaaccca
480ctcgatg aggcacagct tgataaggca accgttcgcc tcatggcaaa
ggttccaatg ctg540gctg cgtacgcaca ccgcgcacgc aagggtgctc
cttacatgta cccagacaac tccctc600a acgcgcgtga gaatttctg
cgcatgatgt tcggttacc aaccgagcca tacgagatc6 60gacccaat
catggtcaag gctctggaca agctgtcat cctgcacgct gaccacgagc
ag720aactg ctccacctcc accgttcgta tgatcggttc cgcacaggcc
aacatgtttg tctcc780at cgctggtggc atcaacgctc tgtccggccc
actgcacggt ggcgcaaacc aggtgtt84 0ctggagatg ctccaagaca
tcaagaacaa ccacggtggc gacgcaaccg cgttcatgaa c900aaggtc
aagaacaagg aagacggcgt ccgcctcatg ggcttcggac accgcgttta
caag960aac tacgatccac gtgcagcaat cgtcaaggag accgcacacg
agatcctcga gcacctc102 0ggtggcgac gatcttctgg atctggcaat
caagctggaa gaaattgcac tggctgatga t1080tactt catctcccgc
aagctctacc cgaacgtaga cttctacacc ggctgatct accgc1140g
caatgggctt cccaactgac ttcttcaccg tattgttcgc aatcggtcgt
ctgccaggal 200tggatcg ctactaccg cgagcagctc ggtgcagcag
gcaacaagat caaccgcca cgc1260cag gtctacaccg gcaaggaatc
ccgcaagttg gttctcgcg aggagcgcta a1314
```

WARNING: possibly wrong combination

command: blastn

query: /bio/local/WWW/pub/tmp/blast.103360/blast.tmp (Not FASTA Format)

database: nr-nt (nucl)

command	query	database
blastp	prot	prot
blastn	nucl	nucl
blastx	nucl	prot
tblastn	prot	nucl
tblastx	nucl	nucl

BLASTN 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= query

(1314 letters)

Database: nr-nt: Non-redundant nucleic acid sequence database Release
05-01-04

46,340,936 sequences; 80,264,366,952 total letters

Searching.....done

Sequences producing significant alignments:

	Score (bits)	E Value
--	-----------------	------------

Top 10

<input checked="" type="checkbox"/> emb:BD094212 [BD094212] Genes for heat resistant enzymes of amin...	2605	0.0
<input checked="" type="checkbox"/> gb:AP005276 [AP005276] Corynebacterium glutamicum ATCC 13032 DNA...	2557	0.0
<input checked="" type="checkbox"/> emb:AX127145 [AX127145] Sequence 7061 from Patent EP1108790.	2557	0.0
<input checked="" type="checkbox"/> emb:AX065419 [AX065419] Sequence 545 from Patent W00100844.	2557	0.0
<input checked="" type="checkbox"/> emb:CGGLTG [X66112] C. glutamicum glt gene for citrate synthase a...	2557	0.0
<input checked="" type="checkbox"/> emb:BX927150 [BX927150] Corynebacterium glutamicum ATCC 13032, I...	2557	0.0
<input checked="" type="checkbox"/> gbu:BA000036 [BA000036] Corynebacterium glutamicum ATCC 13032 DN...	2557	0.0
<input checked="" type="checkbox"/> emb:BD165642 [BD165642] Novel polynucleotide.	2551	0.0
<input checked="" type="checkbox"/> emb:AX123525 [AX123525] Sequence 3441 from Patent EP1108790.	2551	0.0
<input checked="" type="checkbox"/> gb:AP005217 [AP005217] Corynebacterium efficiens YS-314 DNA, com...	1110	0.0

>[emb:BD094212](#) [BD094212] Genes for heat resistant enzymes of amino acid biosynthetic pathway derived from thermophilic coryneform bacteria.
Length = 1314



Top

Score = 2605 bits (1314), Expect = 0.0
Identities = 1314/1314 (100%)
Strand = Plus / Plus

```
Query: 1      atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactacccggt 60
              |||
Sbjct: 1      atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactacccggt 60

Query: 61      ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacgggtgttgcctgggc 120
              |||
Sbjct: 61      ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacgggtgttgcctgggc 120

Query: 121     aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
              |||
Sbjct: 121     aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180

Query: 181     accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgcggctat 240
              |||
Sbjct: 181     accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgcggctat 240

Query: 241     gacatcgctgatctggctgagaatgccacottcaacgaggtttcttacctacttatcaac 300
              |||
Sbjct: 241     gacatcgctgatctggctgagaatgccacottcaacgaggtttcttacctacttatcaac 300

Query: 301     ggtgaactaccaacccagatgagcttcacaagttaacgacgagattcgccaccacacc 360
              |||
Sbjct: 301     ggtgaactaccaacccagatgagcttcacaagttaacgacgagattcgccaccacacc 360
```

Query: 361 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgctcacccaatg 420
|||||
Sbjct: 361 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgctcacccaatg 420

Query: 421 gcaaccttggcttcctcggttaacattttgtctacctactaccaggatcagctgaacca 480
|||||
Sbjct: 421 gcaaccttggcttcctcggttaacattttgtctacctactaccaggatcagctgaacca 480

Query: 481 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaagggttccaatgctg 540
|||||
Sbjct: 481 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaagggttccaatgctg 540

Query: 541 gctgcgtacgcacaccgcgcacgcaagggtgctccttacatgtaccagacaactccctc 600
|||||
Sbjct: 541 gctgcgtacgcacaccgcgcacgcaagggtgctccttacatgtaccagacaactccctc 600

Query: 601 aacgcgcgtgagaacttcctgcgcatgatgttcggttaccgaaccgagccatacagagatc 660
|||||
Sbjct: 601 aacgcgcgtgagaacttcctgcgcatgatgttcggttaccgaaccgagccatacagagatc 660

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
|||||
Sbjct: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
|||||
Sbjct: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780

Query: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840
|||||
Sbjct: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840

Query: 841 ctggagatgctcgaagacatcaagaacaaccacggtggcgacgcaaccgcgttcataaac 900
|||||
Sbjct: 841 ctggagatgctcgaagacatcaagaacaaccacggtggcgacgcaaccgcgttcataaac 900

Query: 901 aaggtcaagaacaaggaagacggcgtccgcctcatgggcttcggacaccgcgtttacaag 960
|||||
Sbjct: 901 aaggtcaagaacaaggaagacggcgtccgcctcatgggcttcggacaccgcgtttacaag 960

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
|||||
Sbjct: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020


Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080
|||||
Sbjct: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080

Query: 1081 tacttcatctcccgcaagctctacccgaacgtagacttctacaccggcctgatctaccgc 1140
|||||
Sbjct: 1081 tacttcatctcccgcaagctctacccgaacgtagacttctacaccggcctgatctaccgc 1140

Query: 1141 gcaatgggcttcccaactgactttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200
|||||
Sbjct: 1141 gcaatgggcttcccaactgactttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200

Query: 1201 tggatcgctcactaccgcgagcagctcgggtgcagcaggcaacaagatcaaccgcccacgc 1260
|||||
Sbjct: 1201 tggatcgctcactaccgcgagcagctcgggtgcagcaggcaacaagatcaaccgcccacgc 1260

Query: 1261 caggctctacaccggcaaggaatcccgaagttggttcctcgcgaggagcgctaa 1314
|||||
Sbjct: 1261 caggctctacaccggcaaggaatcccgaagttggttcctcgcgaggagcgctaa 1314

>gb:AP005276 [AP005276] Corynebacterium glutamicum ATCC 13032 DNA, complete genome,  Top
section 3/10.
Length = 332050

Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

Query: 1 atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactacccggt 60
|||||
Sbjct: 209888 atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactacccggt 209947

Query: 61 ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacgggtgtgtcctgggc 120
|||||
Sbjct: 209948 ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacgggtgtgtcctgggc 210007

Query: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
|||||
Sbjct: 210008 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 210067

Query: 181 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttacgcggctat 240
|||||
Sbjct: 210068 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttacgcggctat 210127

Query: 241 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300
|||||
Sbjct: 210128 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 210187

Query: 301 ggtgaactaccaacccagatgagcttcacaagttaacgacgagattcgccaccacacc 360
|||||
Sbjct: 210188 ggtgagctaccaacccagatgagcttcacaagttaacgacgagattcgccaccacacc 210247

Query: 361 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgtcacccaatg 420
|||||
Sbjct: 210248 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgtcacccaatg 210307

Query: 421 gcaacottggcttctcgtgtaacattttgtctacctactaccaggatcagctgaaccca 480
|||||
Sbjct: 210308 gcaacottggcttctcgtgtaacattttgtctacctactaccaggatcagctgaaccca 210367

Query: 481 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 540
 |||
Sbjct: 210368 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 210427

Query: 541 gctgcgtacgcacaccgcgcacgcaagggtgctccttacatgtaccagacaactccctc 600
 |||
Sbjct: 210428 gctgcgtacgcacaccgcgcacgcaagggtgctccttacatgtaccagacaactccctc 210487

Query: 601 aacgcgcgtgagaacttctcgcatgatgttcggttaccgaaccgagccatacagagatc 660
 ||
Sbjct: 210488 aatgcgcgtgagaacttctcgcatgatgttcggttaccgaaccgagccatacagagatc 210547

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
 |||
Sbjct: 210548 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 210607

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
 |||
Sbjct: 210608 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 210667

Query: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840
 |||
Sbjct: 210668 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 210727

Query: 841 ctggagatgctcgaagacatcaagaacaaccacggtggcgacgcaaccggttcattgaac 900
 |||
Sbjct: 210728 ctggagatgctcgaagacatcaagagcaaccacggtggcgacgcaaccgagttcatgaac 210787

Query: 901 aaggtcaagaacaaggaagacggcgtccgcctcatgggcttcggacaccggtttacaag 960
 |||
Sbjct: 210788 aaggtcaagaacaaggaagacggcgtccgcctcatgggcttcggacaccggtttacaag 210847

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
 |||
Sbjct: 210848 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 210907

Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080
 |||
Sbjct: 210908 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 210967

Query: 1081 tacttcatctcccgcaagctctacccgaacgtagacttctacaccggcctgatctaccgc 1140
 |||
Sbjct: 210968 tacttcatctcccgcaagctctacccgaacgtagacttctacaccggcctgatctaccgc 211027

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200
 |||
Sbjct: 211028 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 211087

Query: 1201 tggatcgctcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 1260
 |||
Sbjct: 211088 tggatcgctcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 211147

Query: 1261 cagggtctacaccggcaaggaatcccgaagttggttcctcgcgaggagcgctaa 1314
|||||
Sbjct: 211148 cagggtctacaccggcaaggaatcccgaagttggttcctcgcgaggagcgctaa 211201

>emb:AX127145 [AX127145] Sequence 7061 from Patent EP1108790.
Length = 349980



Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

Query: 1 atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactaccccggt 60
|||||
Sbjct: 277838 atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactaccccggt 277897

Query: 61 ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacgggtgttgcctgggc 120
|||||
Sbjct: 277898 ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacgggtgttgcctgggc 277957

Query: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
|||||
Sbjct: 277958 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 278017

Query: 181 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttacgcggctat 240
|||||
Sbjct: 278018 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttacgcggctat 278077

Query: 241 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300
|||||
Sbjct: 278078 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 278137

Query: 301 ggtgaactaccaacccagatgagcttcacaagttaacgacgagattcgccaccacacc 360
|||||
Sbjct: 278138 ggtgagctaccaacccagatgagcttcacaagttaacgacgagattcgccaccacacc 278197

Query: 361 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgtcacccaatg 420
|||||
Sbjct: 278198 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgtcacccaatg 278257

Query: 421 gcaaccttggcttctcgttgaacattttgtctacctactaccaggatcagctgaaccca 480
|||||
Sbjct: 278258 gcaaccttggcttctcgttgaacattttgtctacctactaccaggatcagctgaaccca 278317

Query: 481 ctcatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 540
|||||
Sbjct: 278318 ctcatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 278377

Query: 541 gctgcgtacgcacaccgcgcacgaagggtgctccttacatgtaccagacaactccctc 600
|||||
Sbjct: 278378 gctgcgtacgcacaccgcgcacgaagggtgctccttacatgtaccagacaactccctc 278437

Query: 601 aacgcgcgtgagaacttctgcgcatgatgttoggttacccaaccgagccatacagagatc 660
|||
Sbjct: 278438 aatgcgcgtgagaacttctgcgcatgatgttoggttacccaaccgagccatacagagatc 278497

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
|||
Sbjct: 278498 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 278557

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
|||
Sbjct: 278558 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 278617

Query: 781 atcgctggtggcatcaacgctctgtccggcccactgcacggtggcgcaaaccaggctgtt 840
|||
Sbjct: 278618 atcgctggtggcatcaacgctctgtccggcccactgcacggtggcgcaaaccaggctgtt 278677

Query: 841 ctggagatgctcgaagacatcaagaacaaccacggtggcgacgcaaccgcgttcataaac 900
|||
Sbjct: 278678 ctggagatgctcgaagacatcaagagcaaccacggtggcgacgcaaccgcgttcataaac 278737

Query: 901 aaggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 960
|||
Sbjct: 278738 aaggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 278797

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
|||
Sbjct: 278798 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 278857

Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080
|||
Sbjct: 278858 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 278917

Query: 1081 tacttcatctcccgcaagctctaccggaacgtagacttctacaccggcctgatctaccgc 1140
|||
Sbjct: 278918 tacttcatctcccgcaagctctaccggaacgtagacttctacaccggcctgatctaccgc 278977

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200
|||
Sbjct: 278978 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 279037

Query: 1201 tggatcgtcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 1260
|||
Sbjct: 279038 tggatcgtcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 279097

Query: 1261 caggctacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgctaa 1314
|||
Sbjct: 279098 caggctacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgctaa 279151

>emb:AX065419 [AX065419] Sequence 545 from Patent W00100844.
Length = 1416



Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

```
Query: 1   atgtttgaaaggatatactgtggctactgataacaacaaggctgtcctgcactaccccggt 60
          |||
Sbjct: 83   atgtttgaaaggatatactgtggctactgataacaacaaggctgtcctgcactaccccggt 142

Query: 61   ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacggtgttgctcctgggc 120
          |||
Sbjct: 143  ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacggtgttgctcctgggc 202

Query: 121  aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
          |||
Sbjct: 203  aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 262

Query: 181  accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgcggctat 240
          |||
Sbjct: 263  accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgcggctat 322

Query: 241  gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300
          |||
Sbjct: 323  gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 382

Query: 301  ggtgaactaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 360
          |||
Sbjct: 383  ggtgagctaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 442

Query: 361  cttctggacgaggacttcaagtcccagttcaacgtgttccacgcgacgctcacccaatg 420
          |||
Sbjct: 443  cttctggacgaggacttcaagtcccagttcaacgtgttccacgcgacgctcacccaatg 502

Query: 421  gcaaccttggttctcctcggttaacattttgtctacctactaccaggatcagctgaacca 480
          |||
Sbjct: 503  gcaaccttggttctcctcggttaacattttgtctacctactaccaggaccagctgaacca 562

Query: 481  ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 540
          |||
Sbjct: 563  ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 622

Query: 541  gctgcgtacgcacaccgcgcacgcaagggtgctccttacatgtaccagacaactccctc 600
          |||
Sbjct: 623  gctgcgtacgcacaccgcgcacgcaagggtgctccttacatgtaccagacaactccctc 682

Query: 601  aacgcgcgtgagaacttctcctgcgcgatgatgttcggttacccaaccgagccatacagatc 660
          |||
Sbjct: 683  aatgcgcgtgagaacttctcctgcgcgatgatgttcggttacccaaccgagccatacagatc 742

Query: 661  gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
          |||
Sbjct: 743  gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 802
```

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
|||||
Sbjct: 803 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 862

Query: 781 atcgctggtggcatcaacgctctgtccggcccactgcacggtggcgcaaaccaggctgtt 840
|||||
Sbjct: 863 atcgctggtggcatcaacgctctgtccggcccactgcacggtggcgcaaaccaggctgtt 922

Query: 841 ctggagatgctcgaagacatcaagaacaaccacgggtggcgacgcaaccgcgttcataaac 900
|||||
Sbjct: 923 ctggagatgctcgaagacatcaagagcaaccacgggtggcgacgcaaccgcgttcataaac 982

Query: 901 aaggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 960
|||||
Sbjct: 983 aaggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 1042

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
|||||
Sbjct: 1043 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1102

Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080
|||||
Sbjct: 1103 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1162

Query: 1081 tacttcatctcccgcaagctctacccgaacgtagacttctacaccggcctgatctaccgc 1140
|||||
Sbjct: 1163 tacttcatctcccgcaagctctacccgaacgtagacttctacaccggcctgatctaccgc 1222

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggctcgtctgccagga 1200
|||||
Sbjct: 1223 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggctcgtctgccagga 1282

Query: 1201 tggatcgctcactaccgagcagctcggtgcagcaggcaacaagatcaaccgccacgc 1260
|||||
Sbjct: 1283 tggatcgctcactaccgagcagctcggtgcagcaggcaacaagatcaaccgccacgc 1342

Query: 1261 caggcttacaccggcaaggaatcccgcaagttggttcctcgaggagcgctaa 1314
|||||
Sbjct: 1343 caggcttacaccggcaaggaatcccgcaagttggttcctcgaggagcgctaa 1396

>emb:CGGLTG [X66112] C. glutamicum glt gene for citrate synthase and ORF
Length = 3013



Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

Query: 1 atgtttgaaaggatctgtggctactgataacaacaaggctgtcctgcactacccgggt 60
|||||
Sbjct: 838 atgtttgaaaggatctgtggctactgataacaacaaggctgtcctgcactacccgggt 897

Query: 61 ggcgagttcgaatggacatcatcgaggcttctgagggtacaacggtgttgctcctgggc 120
|||||
Sbjct: 898 ggcgagttcgaatggacatcatcgaggcttctgagggtacaacggtgttgctcctgggc 957

Query: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
|||||
Sbjct: 958 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 1017

Query: 181 accgagtcgaagatcacctacatcgatggcgatgcggaatcctgcgttaccgaggctat 240
|||||
Sbjct: 1018 accgagtcgaagatcacctacatcgatggcgatgcggaatcctgcgttaccgaggctat 1077

Query: 241 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300
|||||
Sbjct: 1078 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 1137

Query: 301 ggtgaactaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 360
|||||
Sbjct: 1138 ggtgagctaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 1197

Query: 361 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgctcacccaatg 420
|||||
Sbjct: 1198 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgctcacccaatg 1257

Query: 421 gcaacottggcttcctcggttaacattttgtctacctactaccaggatcagctgaaccca 480
|||||
Sbjct: 1258 gcaacottggcttcctcggttaacattttgtctacctactaccaggaccagctgaaccca 1317

Query: 481 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 540
|||||
Sbjct: 1318 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 1377

Query: 541 gctgcgtacgcacaccgcgacgcaagggtgctccttacatgtaccagacaactccctc 600
|||||
Sbjct: 1378 gctgcgtacgcacaccgcgacgcaagggtgctccttacatgtaccagacaactccctc 1437

Query: 601 aacgcgctgagaacttcctgcgcatgatgttcggttaccgaaccgagccatacagatc 660
|| |||||
Sbjct: 1438 aatgcgctgagaacttcctgcgcatgatgttcggttaccgaaccgagccatacagatc 1497

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
|||||
Sbjct: 1498 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 1557

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
|||||
Sbjct: 1558 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 1617

Query: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840
|||||
Sbjct: 1618 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 1677

Query: 841 ctggagatgctcgaagacatcaagaacaaccacgggtggcgacgcaaccgcgttcacgaac 900
|||||
Sbjct: 1678 ctggagatgctcgaagacatcaagagcaaccacgggtggcgacgcaaccgagttcatgaac 1737

Query: 901 aaggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 960
|||||
Sbjct: 1738 aaggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 1797

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
|||||
Sbjct: 1798 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1857


Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080
|||||
Sbjct: 1858 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1917

Query: 1081 tacttcatctcccgcaagctctaccgcaacgtagacttctacaccggcctgatctaccgc 1140
|||||
Sbjct: 1918 tacttcatctcccgcaagctctaccgcaacgtagacttctacaccggcctgatctaccgc 1977

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200
|||||
Sbjct: 1978 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 2037

Query: 1201 tggatcgctcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgccacgc 1260
|||||
Sbjct: 2038 tggatcgctcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgccacgc 2097

Query: 1261 caggtctacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgctaa 1314
|||||
Sbjct: 2098 caggtctacaccggcaacgaatcccgcaagttggttcctcgcgaggagcgctaa 2151

>emb:BX927150 [BX927150] *Corynebacterium glutamicum* ATCC 13032, IS fingerprint type  Top
4-5, complete genome; segment 3/10
Length = 348475

Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

Query: 1 atgtttgaaaggatatcgtggctactgataacaacaaggctgtcctgcactaccccggt 60
|||||
Sbjct: 181451 atgtttgaaaggatatcgtggctactgataacaacaaggctgtcctgcactaccccggt 181510

Query: 61 ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacgggtgtgtcctgggc 120
|||||
Sbjct: 181511 ggcgagttcgaaatggacatcatcgaggcttctgagggtacaacgggtgtgtcctgggc 181570

Query: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
|||||
Sbjct: 181571 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 181630

Query: 181 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgaggctat 240
|||||
Sbjct: 181631 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgaggctat 181690

Query: 241 gacatcgctgatctggctgagaatgccacctcaacgaggtttcttacctacttatcaac 300
|||||
Sbjct: 181691 gacatcgctgatctggctgagaatgccacctcaacgaggtttcttacctacttatcaac 181750

Query: 301 ggtgaactaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 360
|||||
Sbjct: 181751 ggtgagctaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 181810

Query: 361 cttctggacgaggacttcaagtcccagttcaacgtgttccacgcgacgctcacccaatg 420
|||||
Sbjct: 181811 cttctggacgaggacttcaagtcccagttcaacgtgttccacgcgacgctcacccaatg 181870

Query: 421 gcaaccttggcttcctcggttaacattttgtctactactaccaggatcagctgaaccca 480
|||||
Sbjct: 181871 gcaaccttggcttcctcggttaacattttgtctactactaccaggaccagctgaaccca 181930

Query: 481 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 540
|||||
Sbjct: 181931 ctcgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 181990

Query: 541 gctgcgtacgcacaccgcgcacgaagggtgctccttacatgtaccagacaactccctc 600
|||||
Sbjct: 181991 gctgcgtacgcacaccgcgcacgaagggtgctccttacatgtaccagacaactccctc 182050

Query: 601 aacgcgcgtgagaacttctcgcatgatgttcggttacccaaccgagccatacagatc 660
||
Sbjct: 182051 aatgcgcgtgagaacttctcgcatgatgttcggttacccaaccgagccatacagatc 182110

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
|||||
Sbjct: 182111 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 182170

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
|||||
Sbjct: 182171 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 182230

Query: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840
|||||
Sbjct: 182231 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 182290

Query: 841 ctggagatgctcgaagacatcaagaacaaccacggtggcgacgaaccgcgttcatgaac 900
|||||
Sbjct: 182291 ctggagatgctcgaagacatcaagagcaaccacggtggcgacgaaccgagttcatgaac 182350

Query: 901 aaggtaagaacaaggaagacggcgtccgcctcatgggcttcggacaccgcgtttacaag 960
|||||
Sbjct: 182351 aaggtaagaacaaggaagacggcgtccgcctcatgggcttcggacaccgcgtttacaag 182410

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
|||||
Sbjct: 182411 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 182470


Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080
|||||
Sbjct: 182471 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 182530

Query: 1081 tacttcatctcccgcaagctctaccggaacgtagacttctacaccggcctgatctaccgc 1140
|||||
Sbjct: 182531 tacttcatctcccgcaagctctaccggaacgtagacttctacaccggcctgatctaccgc 182590

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200
|||||
Sbjct: 182591 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 182650

Query: 1201 tggatcgctcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 1260
|||||
Sbjct: 182651 tggatcgctcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 182710

Query: 1261 caggctacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgctaa 1314
|||||
Sbjct: 182711 caggctacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgctaa 182764

>gbu:BA000036 [BA000036] Corynebacterium glutamicum ATCC 13032 DNA, complete genome.  Top
Length = 3309401

Score = 2557 bits (1290), Expect = 0.0
Identities = 1308/1314 (99%)
Strand = Plus / Plus

Query: 1 atgtttgaaaggatctcgtggctactgataacaacaaggctgtcctgcactaccccggt 60
|||||
Sbjct: 877838 atgtttgaaaggatctcgtggctactgataacaacaaggctgtcctgcactaccccggt 877897

Query: 61 ggcgagttcgaaatggacatcatcgaggcttctgagggttaacaacggtgtgtcctgggc 120
|||||
Sbjct: 877898 ggcgagttcgaaatggacatcatcgaggcttctgagggttaacaacggtgtgtcctgggc 877957

Query: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
|||||
Sbjct: 877958 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 878017

Query: 181 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttacccgggctat 240
|||||
Sbjct: 878018 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttacccgggctat 878077

Query: 241 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300
|||||
Sbjct: 878078 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 878137

Query: 301 ggtgaactaccaaccccagatgagcttcacaagtttaacgacgagattcgccaccacacc 360
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878138 ggtgagctaccaaccccagatgagcttcacaagtttaacgacgagattcgccaccacacc 878197

Query: 361 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgctcacccaatg 420
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878198 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgctcacccaatg 878257

Query: 421 gcaaccttggcttcctcggttaacattttgtctacactaccaggatcagctgaaccca 480
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878258 gcaaccttggcttcctcggttaacattttgtctacactaccaggaccagctgaaccca 878317

Query: 481 ctogatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 540
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878318 ctogatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctg 878377

Query: 541 gctgcgtacgcacaccgcgcacgaagggtgctccttacatgtacccagacaactccctc 600
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878378 gctgcgtacgcacaccgcgcacgaagggtgctccttacatgtacccagacaactccctc 878437

Query: 601 aacgcgcgtgagaacttcctgcgcatgatgttcggttacccaaccgagccatacagatc 660
|| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878438 aatgcgcgtgagaacttcctgcgcatgatgttcggttacccaaccgagccatacagatc 878497

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878498 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 878557

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878558 aactgctccacctccaccgttcgtatgatcggttcgcacaggccaacatgtttgtctcc 878617

Query: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878618 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 878677

Query: 841 ctggagatgctcgaagacatcaagaacaaccacggtggcgacgcaaccgcgttcataaac 900
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878678 ctggagatgctcgaagacatcaagagcaaccacggtggcgacgcaaccgagttcatgaac 878737

Query: 901 aaggtcaagaacaaggaagacggcgtccgcctcatgggcttcggacaccgcgtttacaag 960
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878738 aaggtcaagaacaaggaagacggcgtccgcctcatgggcttcggacaccgcgtttacaag 878797

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctogagcacctc 1020
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878798 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctogagcacctc 878857

Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Sbjct: 878858 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 878917

Query: 1081 tacttcatctcccgcaagctctacccgaacgtagacttctacaccggcctgatctaccgc 1140
|||||
Sbjct: 878918 tacttcatctcccgcaagctctacccgaacgtagacttctacaccggcctgatctaccgc 878977

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggctcgtctgccagga 1200
|||||
Sbjct: 878978 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggctcgtctgccagga 879037

Query: 1201 tggatcgctcactaccgagcagctcgggtgcagcaggcaacaagatcaaccgcccacgc 1260
|||||
Sbjct: 879038 tggatcgctcactaccgagcagctcgggtgcagcaggcaacaagatcaaccgcccacgc 879097

Query: 1261 caggcttacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgctaa 1314
|||||
Sbjct: 879098 caggcttacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgctaa 879151

>emb:BD165642 [BD165642] Novel polynucleotide.
Length = 1311



Top

Score = 2551 bits (1287), Expect = 0.0
Identities = 1305/1311 (99%)
Strand = Plus / Plus

Query: 1 atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactaccccggt 60
|||||
Sbjct: 1 atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactaccccggt 60

Query: 61 ggcgagttcgaaatggacatcatcgaggcttctgagggttaacaacgggtgttgcctgggc 120
|||||
Sbjct: 61 ggcgagttcgaaatggacatcatcgaggcttctgagggttaacaacgggtgttgcctgggc 120

Query: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
|||||
Sbjct: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180

Query: 181 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgcggtat 240
|||||
Sbjct: 181 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgcggtat 240

Query: 241 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300
|||||
Sbjct: 241 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300

Query: 301 ggtgaactaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 360
|||||
Sbjct: 301 ggtgagctaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 360

Query: 361 cttctggacgaggacttcaagtcacgttcaacgtgttccacgcgacgctcaccgaatg 420
|||||
Sbjct: 361 cttctggacgaggacttcaagtcacgttcaacgtgttccacgcgacgctcaccgaatg 420

Query: 421 gcaaccttggcttcctcggttaacattttgtctacctactaccaggatcagctgaaccca 480
|||||
Sbjct: 421 gcaaccttggcttcctcggttaacattttgtctacctactaccaggaccagctgaaccca 480

Query: 481 ctcgatgaggcacagcttgataaggcaaccggttcgcctcatggcaaagggttccaatgctg 540
|||||
Sbjct: 481 ctcgatgaggcacagcttgataaggcaaccggttcgcctcatggcaaagggttccaatgctg 540

Query: 541 gctggtacgcacaccgcgcacgcaagggtgctccttacatgtaccagacaactccctc 600
|||||
Sbjct: 541 gctggtacgcacaccgcgcacgcaagggtgctccttacatgtaccagacaactccctc 600

Query: 601 aacgcgctgagaacttcctgcgcatgatgttcggttacccaaccgagccatacagagatc 660
|| |||||
Sbjct: 601 aatgcgctgagaacttcctgcgcatgatgttcggttacccaaccgagccatacagagatc 660

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
|||||
Sbjct: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720

Query: 721 aactgctccacctccacggttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780
|||||
Sbjct: 721 aactgctccacctccacggttcgtatgatcggttcgcacaggccaacatgtttgtctcc 780

Query: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840
|||||
Sbjct: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840

Query: 841 ctggagatgctcgaagacatcaagaacaaccacggtggcgacgcaaccgcgttcataaac 900
|||||
Sbjct: 841 ctggagatgctcgaagacatcaagagcaaccacggtggcgacgcaaccgagttcatgaac 900

Query: 901 aaggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 960
|||||
Sbjct: 901 aaggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 960

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
|||||
Sbjct: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020

Query: 1021 ggtggcgacgatcttctggtatctggcaatcaagctggaagaaattgcactggctgatgat 1080
|||||
Sbjct: 1021 ggtggcgacgatcttctggtatctggcaatcaagctggaagaaattgcactggctgatgat 1080

Query: 1081 tacttcatctcccgcaagctctaccggaacgtagacttctacaccggcctgatctaccgc 1140
|||||
Sbjct: 1081 tacttcatctcccgcaagctctaccggaacgtagacttctacaccggcctgatctaccgc 1140

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200
|||||
Sbjct: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200

Query: 1201 tggatcgctcactaccgagcagctcgggtgcagcaggcaacaagatcaaccgcccacgc 1260
|||||
Sbjct: 1201 tggatcgctcactaccgagcagctcgggtgcagcaggcaacaagatcaaccgcccacgc 1260

Query: 1261 caggctctacaccggcaaggaatcccgaagttggttcctcgcgaggagcgc 1311
|||||
Sbjct: 1261 caggctctacaccggcaaggaatcccgaagttggttcctcgcgaggagcgc 1311

>emb:AX123525 [AX123525] Sequence 3441 from Patent EP1108790.
Length = 1311

[Top](#)

Score = 2551 bits (1287), Expect = 0.0
Identities = 1305/1311 (99%)
Strand = Plus / Plus

Query: 1 atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactaccccggt 60
|||||
Sbjct: 1 atgtttgaaagggatatcgtggctactgataacaacaaggctgtcctgcactaccccggt 60

Query: 61 ggcgagttcgaaatggacatcatcgaggcttctgagggttaacaacggtgttgcctgggc 120
|||||
Sbjct: 61 ggcgagttcgaaatggacatcatcgaggcttctgagggttaacaacggtgttgcctgggc 120

Query: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180
|||||
Sbjct: 121 aagatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctcc 180

Query: 181 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttacccgggctat 240
|||||
Sbjct: 181 accgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttacccgggctat 240

Query: 241 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300
|||||
Sbjct: 241 gacatcgctgatctggctgagaatgccaccttcaacgaggtttcttacctacttatcaac 300

Query: 301 ggtgaactaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 360
|||||
Sbjct: 301 ggtgagctaccaacccagatgagcttcacaagtttaacgacgagattcgccaccacacc 360

Query: 361 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgtcacccaatg 420
|||||
Sbjct: 361 cttctggacgaggacttcaagtcccagttcaacgtgttcccacgcgacgtcacccaatg 420

Query: 421 gcaaccttggttcctcgtgtaacattttgtctacctactaccaggatcagctgaaccca 480
|||||
Sbjct: 421 gcaaccttggttcctcgtgtaacattttgtctacctactaccaggaccagctgaaccca 480

Query: 481 ctcgatgaggcacagcttgataaaggcaaccgttcgcctcatggcaaaggttccaatgctg 540
|||||
Sbjct: 481 ctcgatgaggcacagcttgataaaggcaaccgttcgcctcatggcaaaggttccaatgctg 540

Query: 541 gctgcgtacgcacaccgcgcacgcaagggtgctccttacatgtacccagacaactccctc 600
|||||
Sbjct: 541 gctgcgtacgcacaccgcgcacgcaagggtgctccttacatgtacccagacaactccctc 600

Query: 601 aacgcgcgtgagaacttcctgcgcgatgatgttcggttacccaaccgagccatacagatc 660
|| |||||
Sbjct: 601 aatgcgcgtgagaacttcctgcgcgatgatgttcggttacccaaccgagccatacagatc 660

Query: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720
|||||
Sbjct: 661 gacccaatcatggtcaaggctctggacaagctgctcatcctgcacgctgaccacgagcag 720

Query: 721 aactgctccacctccaccgttcgtatgatcggttcgcgcacaggccaacatgtttgtctcc 780
|||||
Sbjct: 721 aactgctccacctccaccgttcgtatgatcggttcgcgcacaggccaacatgtttgtctcc 780

Query: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840
|||||
Sbjct: 781 atcgctggtggcatcaacgctctgtccggccactgcacggtggcgcaaaccaggctgtt 840

Query: 841 ctggagatgctcgaagacatcaagaacaaccacgggtggcgacgcaaccgcgttcatgaac 900
|||||
Sbjct: 841 ctggagatgctcgaagacatcaagagcaaccacgggtggcgacgcaaccgagttcatgaac 900

Query: 901 aagggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 960
|||||
Sbjct: 901 aagggtcaagaacaaggaagacggcgctccgcctcatgggcttcggacaccgcgtttacaag 960

Query: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020
|||||
Sbjct: 961 aactacgatccacgtgcagcaatcgtcaaggagaccgcacacgagatcctcgagcacctc 1020


Query: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080
|||||
Sbjct: 1021 ggtggcgacgatcttctggatctggcaatcaagctggaagaaattgcactggctgatgat 1080

Query: 1081 tacttcatctcccgcaagctctaccgcaacgtagacttctacaccggcctgatctaccgc 1140
|||||
Sbjct: 1081 tacttcatctcccgcaagctctaccgcaacgtagacttctacaccggcctgatctaccgc 1140

Query: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200
|||||
Sbjct: 1141 gcaatgggcttcccaactgacttcttcaccgtattgttcgcaatcggtcgtctgccagga 1200

Query: 1201 tggatcgctcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 1260
|||||
Sbjct: 1201 tggatcgctcactaccgcgagcagctcggtgcagcaggcaacaagatcaaccgcccacgc 1260

Query: 1261 cagggtctacaccggcaaggaatcccgcaagttggttcctcgcgaggagcgc 1311
|||||
Sbjct: 1261 cagggtctacaccggcaacgaatcccgcaagttggttcctcgcgaggagcgc 1311

>gb:AP005217 [AP005217] *Corynebacterium efficiens* YS-314 DNA, complete genome,  [Top](#)
section 4/11.
Length = 300750

Score = 1110 bits (560), Expect = 0.0
Identities = 1096/1273 (86%), Gaps = 5/1273 (0%)
Strand = Plus / Plus

Query: 3 gtttgaaaggatctctggctactgataacaacaaggctgtcctgcactaccccggtgg 62
|||||
Sbjct: 22750 gtttgaaaggaaatcgtggcttctgataacaacaaggctgtactgcactaccctggcgg 22809

Query: 63 cgagttcgaatggacatcatcgaggcttctgagggttaacaacggtgtgtcctgggcaa 122
||| |||||
Sbjct: 22810 cgaattcgagatgggcatcaagcaggccaccgagggttaactccggtgtcatcctgggtaa 22869

Query: 123 gatgctgtctgagactggactgatcacttttgaccaggttatgtgagcactggctccac 182
|||||
Sbjct: 22870 gatgctgtcggaaaccggtctggtcaccttcgaccccggttatgtcagcaccggttccac 22929

Query: 183 cgagtcgaagatcacctacatcgatggcgatgcgggaatcctgcgttaccgcggtatga 242
||| |||
Sbjct: 22930 cgaatccaagatcacctacatcgatggtgatgcaggcatcctgcgctaccgcggtacga 22989

Query: 243 catcgctgatctggctgagaatgccaccttcaacgaggtttcttacctattatcaacgg 302
||| |||
Sbjct: 22990 cattcgggatctggccgaaaatgccaccttcaatgaggtctcctacctcctgatcaaggg 23049

Query: 303 tgaactaccaaccccagatgagcttcacaagtttaacgacgagattcgccaccacaccct 362
||| |||
Sbjct: 23050 tgagctcccgaccccggaagagctccacaagtttaacgacgagattcgtcaccacaccct 23109

Query: 363 tctggacgaggacttcaagtccagttcaactgttccacgcgacgctcacccaatggc 422
|||||
Sbjct: 23110 gctggacgaggacttcaagtccagttcaatgtcttccctcgcgatgccacccgatggc 23169

Query: 423 aaccttggtctcctcggttaacattttgtctacctactaccaggatcagctgaaccact 482
||| |||
Sbjct: 23170 caccctggcctcctcggttaacatcctctccacctactaccaggatcagctggatcccct 23229

Query: 483 cgatgaggcacagcttgataaggcaaccgttcgcctcatggcaaaggttccaatgctggc 542
|||||
Sbjct: 23230 ggatgaggctcagctggacaaggcaaccgttcgcctcatggcaaaggttccgatgctggc 23289

Query: 543 tgcgtacgcacaccgcgcacgaagggtgtccttacatgtacccagacaactccctcaa 602
||| |||
Sbjct: 23290 tgcatacgcacaccgtgcccgcaagggtgcgcctacatgtacccggacaactccctcaa 23349

Query: 603 cgcgcgtgagaacttctcgcgatgatgttcggttacccaaccgagccatacagagatcga 662
||| |||

Posted date: Jan 4, 2005 6:06 AM
Number of letters in database: 1,999,861,861
Number of sequences in database: 370,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.02
Posted date: Jan 4, 2005 6:13 AM
Number of letters in database: 1,999,963,845
Number of sequences in database: 360,118

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.03
Posted date: Jan 4, 2005 6:28 AM
Number of letters in database: 1,999,999,976
Number of sequences in database: 3,329,958

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.04
Posted date: Jan 4, 2005 6:45 AM
Number of letters in database: 1,999,999,708
Number of sequences in database: 3,404,633

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.05
Posted date: Jan 4, 2005 7:03 AM
Number of letters in database: 1,999,999,998
Number of sequences in database: 3,904,937

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.06
Posted date: Jan 4, 2005 7:23 AM
Number of letters in database: 1,999,999,553
Number of sequences in database: 4,328,864

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.07
Posted date: Jan 4, 2005 7:42 AM
Number of letters in database: 1,999,999,957
Number of sequences in database: 3,891,732

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.08
Posted date: Jan 4, 2005 7:59 AM
Number of letters in database: 1,999,999,671
Number of sequences in database: 3,486,474

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.09
Posted date: Jan 4, 2005 8:23 AM
Number of letters in database: 1,999,999,859
Number of sequences in database: 3,293,154

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.10
Posted date: Jan 4, 2005 8:41 AM
Number of letters in database: 1,999,999,669
Number of sequences in database: 3,828,471

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.11
Posted date: Jan 4, 2005 8:57 AM
Number of letters in database: 1,999,999,424
Number of sequences in database: 2,772,633

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.12
Posted date: Jan 4, 2005 9:05 AM
Number of letters in database: 1,999,921,952
Number of sequences in database: 631,119

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.13
Posted date: Jan 4, 2005 9:13 AM
Number of letters in database: 1,999,956,728
Number of sequences in database: 16,152

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.14

Posted date: Jan 4, 2005 9:19 AM
Number of letters in database: 1,999,893,819
Number of sequences in database: 9139

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.15
Posted date: Jan 4, 2005 9:25 AM
Number of letters in database: 1,999,809,626
Number of sequences in database: 8148

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.16
Posted date: Jan 4, 2005 9:32 AM
Number of letters in database: 1,999,958,517
Number of sequences in database: 9281

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.17
Posted date: Jan 4, 2005 9:39 AM
Number of letters in database: 1,999,869,985
Number of sequences in database: 118,685

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.18
Posted date: Jan 4, 2005 9:46 AM
Number of letters in database: 1,999,869,072
Number of sequences in database: 575,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.19
Posted date: Jan 4, 2005 9:55 AM
Number of letters in database: 1,999,866,894
Number of sequences in database: 705,081

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.20
Posted date: Jan 4, 2005 10:02 AM
Number of letters in database: 1,999,925,325
Number of sequences in database: 63,082

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.21
Posted date: Jan 4, 2005 10:10 AM
Number of letters in database: 1,999,999,826
Number of sequences in database: 569,309

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.22
Posted date: Jan 4, 2005 10:22 AM
Number of letters in database: 1,997,416,774
Number of sequences in database: 2,119,519

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.23
Posted date: Jan 4, 2005 10:29 AM
Number of letters in database: 1,999,944,509
Number of sequences in database: 107,016

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.24
Posted date: Jan 4, 2005 10:36 AM
Number of letters in database: 1,999,998,745
Number of sequences in database: 293,074

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.25
Posted date: Jan 4, 2005 10:45 AM
Number of letters in database: 1,999,996,900
Number of sequences in database: 1,064,738

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.26
Posted date: Jan 4, 2005 10:55 AM
Number of letters in database: 1,999,992,337
Number of sequences in database: 933,438

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.27

Posted date: Jan 4, 2005 11:02 AM
Number of letters in database: 1,999,979,685
Number of sequences in database: 288,812

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.28
Posted date: Jan 4, 2005 11:09 AM
Number of letters in database: 1,999,992,360
Number of sequences in database: 288,789

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.29
Posted date: Jan 4, 2005 11:16 AM
Number of letters in database: 1,999,991,524
Number of sequences in database: 89,111

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.30
Posted date: Jan 4, 2005 11:23 AM
Number of letters in database: 1,999,976,519
Number of sequences in database: 217,802

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.31
Posted date: Jan 4, 2005 11:29 AM
Number of letters in database: 1,999,995,610
Number of sequences in database: 136,831

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.32
Posted date: Jan 4, 2005 11:36 AM
Number of letters in database: 1,999,921,996
Number of sequences in database: 162,607

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.33
Posted date: Jan 4, 2005 11:43 AM
Number of letters in database: 1,999,964,690
Number of sequences in database: 218,162

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.34
Posted date: Jan 4, 2005 11:50 AM
Number of letters in database: 1,999,976,965
Number of sequences in database: 61,666

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.35
Posted date: Jan 4, 2005 11:57 AM
Number of letters in database: 1,999,991,196
Number of sequences in database: 368,188

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.36
Posted date: Jan 4, 2005 12:05 PM
Number of letters in database: 1,999,904,998
Number of sequences in database: 477,581

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.37
Posted date: Jan 4, 2005 12:11 PM
Number of letters in database: 1,999,925,109
Number of sequences in database: 63,652

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.38
Posted date: Jan 4, 2005 12:18 PM
Number of letters in database: 1,999,998,888
Number of sequences in database: 310,761

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.39
Posted date: Jan 4, 2005 12:25 PM
Number of letters in database: 1,998,257,110
Number of sequences in database: 177,152

Database: /bio/db/blast/db/.../fasta/nr-nt/nr-nt.40

Posted date: Jan 4, 2005 12:26 PM
Number of letters in database: 270,246,158
Number of sequences in database: 39,235

Lambda	K	H
1.37	0.711	1.31

Gapped

Lambda	K	H
1.37	0.711	1.31

Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 36,390,912
Number of Sequences: 46340936
Number of extensions: 36390912
Number of successful extensions: 627339
Number of sequences better than 10.0: 220
Number of HSP's better than 10.0 without gapping: 220
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 624290
Number of HSP's gapped (non-prelim): 3035
length of query: 1314
length of database: 80,264,366,952
effective HSP length: 24
effective length of query: 1290
effective length of database: 79,152,184,488
effective search space: 102106317989520
effective search space used: 102106317989520
T: 0
A: 0
X1: 11 (21.8 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 22 (44.1 bits)

=

BLASTP Search Result

Computed at GenomeNet BLAST2 Server (Kyoto Center) on Thu Jan 6 11:02:36 JST 2005

Database Name NR-AA

>query

```

MFERDIVATD NNAVLHYPG GEFEMDIEA SEGNGVVLG KMLSETGLIT
FDPGYVSTGS TESKITYIDG DAGILRYRGY DIADLAENAT FNEVSYLLIN
GELPTDELH KFNDEIRHHT LLEDFKSQF NVFPRDAHPM ATASSVNIL
STYYQDQLNP LDEAQLDKAT VRLMAKVPML AAYHRARKG APYMPDNSL
NARENFLRMM FGYPTEPYEI DPIMVKALDK LLILHADHEQ NCSTSTVRMI
GSAQANMFVS IAGGINALSG PLHGGANQAV LEMLEDIKNN HGGDATAFMN
KVKNKEDGVR LMGFGHRVYK NYDPRAAIVK ETAHEILEHL GGDDLLDLAI
KLEEIALADD YFISRKLYPN VDFYTGLIYR AMGFPTDFFT VLFAIGRLPG
WIAHYREQLG AAGNKINRPR QVYTGKESRK LVPREER*

```

BLASTP 2.2.10 [Oct-19-2004]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= query
(437 letters)

Database: nr-aa: Non-redundant protein sequence database Release
05-01-04

1,848,798 sequences; 600,567,511 total letters

Searching.....done

Sequences producing significant alignments:

	Score (bits)	E Value
--	-----------------	------------

Top 10	Clear	Select operation	Exec
<input checked="" type="checkbox"/> sp:CISY_CORGL [P42457] Citrate synthase (EC 2.3.3.1).>pir:I40717...			855 0.0
<input checked="" type="checkbox"/> gp:AX065419_1 [AX065419] Sequence 545 from Patent W00100844. [Co...			842 0.0
<input checked="" type="checkbox"/> tr:Q8RQP3 [Q8RQP3] Citrate synthase (EC 2.3.3.1).>gpu:BA000035_9...			798 0.0
<input checked="" type="checkbox"/> tr:Q6NIJ0 [Q6NIJ0] Citrate synthase (EC 2.3.3.1).>trnew:CAE49303...			750 0.0
<input checked="" type="checkbox"/> tr:Q9RMRO [Q9RMRO] Citrate synthase.>gp:AF191033_1 [AF191033] ci...			548 e-155
<input checked="" type="checkbox"/> tr:Q5Z238 [Q5Z238] Putative citrate synthase.>gpu:AP006618_661 [...			546 e-154
<input checked="" type="checkbox"/> tr:Q9R339 [Q9R339] Citrate synthase (EC 4.1.3.7).>gpu:SC0939113_...			536 e-151
<input checked="" type="checkbox"/> tr:Q7U122 [Q7U122] PROBABLE CITRATE SYNTHASE I GLTA2 (EC 2.3.3.1...			535 e-150
<input checked="" type="checkbox"/> sp:CISY_MYCTU [Q10530] Citrate synthase 1 (EC 2.3.3.1).>pir:E707...			535 e-150
<input checked="" type="checkbox"/> tr:Q82CL5 [Q82CL5] Putative citrate synthase.>gpu:BA000030_5334 ...			533 e-150

>sp:CISY_CORGL [P42457] Citrate synthase (EC 2.3.3.1).>pir:I40717 [I40717] citrate ▲Top
(si)-synthase (EC 4.1.3.7) - Corynebacterium
glutamicum>prf:2106273A citrate synthase -
Corynebacterium glutamicum>gpu:BA000036_829 [BA000036]
Citrate synthase [Corynebacterium glutamicum ATCC 13032]
Length = 437

Score = 855 bits (2209), Expect = 0.0
Identities = 425/437 (97%), Positives = 426/437 (97%)

Query: 1 MFERDIVATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGS 60
MFERDIVATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGS
Sbjct: 1 MFERDIVATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGS 60

Query: 61 TESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHT 120
TESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHT
Sbjct: 61 TESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHT 120

Query: 121 LLEDEFKSFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPML 180
LLEDEFKSFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPML
Sbjct: 121 LLEDEFKSFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPML 180


Query: 181 AAYAHRARKGAPYMYPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ 240
AAYAHRARKGAPYMYPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ
Sbjct: 181 AAYAHRARKGAPYMYPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQ 240

Query: 241 NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMN 300
NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIK+NHGGDAT FMN
Sbjct: 241 NCSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKSNHGGDATEFMN 300

Query: 301 KVKNKEDGVRLMGFHRVYKNDPRAAIVKETAHEILEHXXXXXXXXXAIKLEEIALADD 360
KVKNKEDGVRLMGFHRVYKNDPRAAIVKETAHEILEH AIKLEEIALADD
Sbjct: 301 KVKNKEDGVRLMGFHRVYKNDPRAAIVKETAHEILEHGGDDLDLAIAIKLEEIALADD 360

Query: 361 YFISRKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPR 420
YFISRKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPR
Sbjct: 361 YFISRKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPR 420

Query: 421 QVYTGKESRKLVPREER 437
QVYTG ESRKLVPREER
Sbjct: 421 QVYTGNESRKLVPREER 437

>gp:AX065419_1 [AX065419] Sequence 545 from Patent W00100844. [Corynebacterium  Top
glutamicum]
Length = 431

Score = 842 bits (2175), Expect = 0.0
Identities = 418/431 (96%), Positives = 420/431 (97%)

Query: 7 VATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
+ATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT
Sbjct: 1 MATDNNKAVLHYPGGEFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 60

Query: 67 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLEDEF 126
YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLEDEF
Sbjct: 61 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLEDEF 120

Query: 127 KSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR 186
KSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR
Sbjct: 121 KSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYAHR 180

Query: 187 ARKGAPYMYPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
ARKGAPYMYPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST
Sbjct: 181 ARKGAPYMYPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKKE 306
VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIK+NHGGDAT FMNKVKKE
Sbjct: 241 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKSNHGGDATEFMNKVKKE 300

Query: 307 DGVRLMGFHRVYKNDPRAAIVKETAHEILEHXXXXXXXXXAIKLEEIALADDYFISRK 366
DGVRLMGFHRVYKNDPRAAIVKETAHEILEH AIKLEEIALADDYFISRK
Sbjct: 301 DGVRLMGFHRVYKNDPRAAIVKETAHEILEHGGDDLDLAIAIKLEEIALADDYFISRK 360

Query: 367 LYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGK 426
LYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTG
Sbjct: 361 LYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGN 420

Query: 427 ESRKLVPREER 437
ESRKLVPREER
Sbjct: 421 ESRKLVPREER 431

>tr:Q8RQP3 [Q8RQP3] Citrate synthase (EC 2.3.3.1).>gpu:BA000035_903 [BA000035] [▲Top](#)
citrate synthase [Corynebacterium efficiens
YS-314]>gp:AB082520_1 [AB082520] citrate synthase
[Corynebacterium efficiens]>gp:AP005217_19 [AP005217]
citrate synthase [Corynebacterium efficiens YS-314]
Length = 470

Score = 798 bits (2060), Expect = 0.0
Identities = 394/436 (90%), Positives = 413/436 (94%), Gaps = 1/436 (0%)

Query: 2 FERDIVATDNNKAVLHYPGGEFEMDIEASEGNNGVVLGKMLSETGLITFDPGYVSTGST 61
FER+IVA+DNNKAVLHYPGGEFEM I +A+EGN+GV+LGKMLSETGL+TFDPGYVSTGST
Sbjct: 36 FERIVASDNNKAVLHYPGGEFEMGIKQATEGNSGVILGKMLSETGLVTFDPGYVSTGST 95

Query: 62 ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTL 121
ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLI GELPTP+ELHKFNDEIRHHTL
Sbjct: 96 ESKITYIDGDAGILRYRGYDIADLAENATFNEVSYLLIKGELPTPEELHKFNDEIRHHTL 155

Query: 122 LDEDFKSQFNVFPRDAHMPATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLA 181
LDEDFKSQFNVFPRDAHMPATLASSVNI LSTYYQDQL+PLDEAQLDKATVRLMAKVPMLA
Sbjct: 156 LDEDFKSQFNVFPRDAHMPATLASSVNI LSTYYQDQLDPLDEAQLDKATVRLMAKVPMLA 215

Query: 182 AYAHRRARKGAPYMPDNSLNARENFLRMMFGYPTPEYEDPIMVKALDKLLILHADHEQN 241
AYAHRRARKGAPYMPDNSLNARENFLRMMFGYPTPEYEDPIMVKALDKLLILHADHEQN
Sbjct: 216 AYAHRRARKGAPYMPDNSLNARENFLRMMFGYPTPEYEDPIMVKALDKLLILHADHEQN 275

Query: 242 CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNK 301
CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLE+I N GGDAT FMN+
Sbjct: 276 CSTSTVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEEIAAN-GGDATDFMNR 334

Query: 302 VKNKEDGVRLMGFGRVYKNDPRAAIVKETAHEILEHXXXXXXXXXA KLEEIALADDY 361
VKNKE GVRMLMGFGRVYKNDPRAAIVK+TAHEILEH A+KLEEIAL DDY
Sbjct: 335 VKNKEGVRLMGFGRVYKNDPRAAIVKDTAHEILEHLGGDPLDLALKLEEIALNDDY 394

Query: 362 FISRKLYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQ 421
FISRKLYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQL G KINRPRQ
Sbjct: 395 FISRKLYPNVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLADPGAKINRPRQ 454

Query: 422 VYTGKESRKLVPREER 437
+YTG+ +RK++PREER
Sbjct: 455 IYTGETARKIIPREER 470

>tr:Q6NIJ0 [Q6NIJ0] Citrate synthase (EC 2.3.3.1).>trnew:CAE49303 [CAE49303] [▲Top](#)
Citrate synthase (EC 2.3.3.1).>gpu:BX248356_61
[BX248356] citrate synthase [Corynebacterium
diphtheriae]>gp:BX248356_61 [BX248356] citrate synthase
[Corynebacterium diphtheriae]
Length = 435

Score = 750 bits (1937), Expect = 0.0
Identities = 371/433 (85%), Positives = 401/433 (92%), Gaps = 3/433 (0%)

Query: 6 IVATDN-NKAVLHYPGGEFEMDIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESK 64

Sbjct: 5 +VAT+N +KAVLHYPGGE+EMDII A+EGN+GVVL K+LS+TG++TFDPGYVSTGSTESK
LVATENKDKAVLHYPGGEYEMDIIHATEGNDGVVLDKLLSQTGMVTFDPGYVSTGSTESK 64

Query: 65 ITYIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDE 124
ITYIDGD GILR+RGYDIADLAENATFNEVSYLLI G LPT DELHKFN+EIRHHTLLDE

Sbjct: 65 ITYIDGDNGILRHRGYDIADLAENATFNEVSYLLIKGHLPTVDELHKFNNEIRHHTLLDE 124

Query: 125 DFKSQFNVPFPRDAHMPATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYA 184
DFKSQFN+FPRAHMP+ LASSVNI LSTYYQDQLNPLDE QLDKATVRL+AKVPMLAAYA

Sbjct: 125 DFKSQFNI FPRDAHMPMSVLASSVNI LSTYYQDQLNPLDEEQLDKATVRLAKVPMLAAYA 184

Query: 185 HRARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCST 244
+RA KGAPYMPDNSLNARENFLRMMFGYPTEPYE+DP++ KALDKLLILHADHEQNCST

Sbjct: 185 YRASKGAPYMPDNSLNARENFLRMMFGYPTEPYEVDPVVAKALDKLLILHADHEQNCST 244

Query: 245 STVRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKN 304
STVRMIGSAQANMFV++AGGINALSGPLHGGANQAVLEMLE+IK N GGDAT FMN+VKN

Sbjct: 245 STVRMIGSAQANMFVAVAGGINALSGPLHGGANQAVLEMLEEIKAN-GGDATDFMNRVKN 303

Query: 305 KEDGVRLMGFGHRVYKNDPRAAIVKETAHEILEHXXXXXXXXXA KLEEIALADDYFIS 364
KE GVRLMGFGHRVYKNDPRAAIVKETAHEILEH A+KLEEIAL+DDYF+S

Sbjct: 304 KEGVRLMGFGHRVYKNDPRAAIVKETAHEILEHLGGDELLDLAMKLEEIALSDDYFVS 363

Query: 365 RKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYT 424
RKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIA YREQL A KINRPRQ+YT

Sbjct: 364 RKLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAQYREQL-ATTTKINRPRQIYT 422

Query: 425 GKESRKLVPREER 437
G+ RK+ PRE+R

Sbjct: 423 GETLRKVTPREQR 435

>tr:Q9RMR0 [Q9RMR0] Citrate synthase.>gp:AF191033_1 [AF191033] citrate
synthase [Mycobacterium smegmatis]
Length = 441

▲Top

Score = 548 bits (1413), Expect = e-155
Identities = 272/421 (64%), Positives = 328/421 (77%), Gaps = 2/421 (0%)

Query: 18 YPGGEFEMDII EASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKITYIDGDAGILRY 77
YPGG+ E+ I++A+EG + V LGK L+ET L TFD G+++T ST+S ITYIDG+ GILRY

Sbjct: 22 YPGGKLELPILKATEGTDSVALGKFLAETNLTFDSGFMNTASTKSAITYIDGEGILRY 81

Query: 78 RGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDFKSQFNVPFPRDA 137
RG I LAE +TF EVSYLLI GELPTP +L +F +I+ HTLL ED K F+ FPR+A

Sbjct: 82 RGIPIEQLAEKSTFIEVSYLLIYGELPTPTQLEEF TTKIQRHTLLHEDLKRFFDGFPRNA 141

Query: 138 HPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHRARKGAPYMPD 197
HPM L+S+VN LS YYQD L+P D+ Q++ +T+RL+AK+P +AAYA++ G P++YPD

Sbjct: 142 HPMPVLSSAVNALSAYYQDSLDPKDDEQVELSTIRLLAKLPTIAAYAYKKSAGQPFYPD 201

Query: 198 NSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTSTVRMIGSAQANM 257
NSL+ ENFLRM FG+P EPYE++P + KALD L ILHADHEQNCSTSTVR++GS+QAN+

Sbjct: 202 NSLSLVENFLRMTFGFPAEPYEVNPDVAKALDMLFILHADHEQNCSTSTVRLVGSSQANL 261

Query: 258 FVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGVRLMGFGHR 317
F SI+GGINAL GPLHGGANQAVLEML+ IK + GGD FM +VKNKE GV+LMGFGHR

Sbjct: 262 FTSISGINALWGPLHGGANQAVLEMLDAIKAD-GGDTKKFMERVKNKEAGVKLMGFGHR 320

Query: 318 VYKNYDPRAAIVKETAHEILEHXXXXXXXXXA K-LEEIALADDYFISRKLYPNVDFYTG 376
VYKNYDPRAAIVK+TA +ILE K LEE+AL DDYFI RKLYPNVDFYTG

Sbjct: 321 VYKNYDPRAAIVKKTADQILETLGVQDDLLEIAKGLEEVALNDDYFIERKLYPNVDFYTG 380

Query: 377 LIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKESRKLVPREE 436

+IYRAMGFPT FTVLFA+GRLPGWIAH+RE KI RPRQ+YTG R VP +
Sbjct: 381 VIYRAMGFPTRMFTVLFA+GRLPGWIAH+REMHEDPTTKIGRPRQLYTGYTERDYVPMSD 440

Query: 437 R 437

R

Sbjct: 441 R 441

>tr:Q5Z238 [Q5Z238] Putative citrate synthase. >gpu:AP006618_661 [AP006618] ▲Top
putative citrate synthase [Nocardia farcinica IFM
10152]>gp:AP006618_661 [AP006618] putative citrate
synthase [Nocardia farcinica]
Length = 433

Score = 546 bits (1406), Expect = e-154

Identities = 270/421 (64%), Positives = 328/421 (77%), Gaps = 3/421 (0%)

Query: 10 DNNKAVLHYPGGEFEMDIIEASEGNGVVLGKMLSETGLITFDPGYVSTGSTESKITYID 69
D+ K VL YPGGE+ M I EA+EGN+G+ LGKML+ TG +T+DPG+++T T+S ITYID
Sbjct: 7 DDAKPVLSYPGGEYAMTITEATEGNHGIDLKMLASTGYVTYDPGFMNTAPTksAITYID 66

Query: 70 GDAGILRYRGYDIADLAENATFNEVSyllINGELPTDELHKFNDEIRHHTLLDEDFKSQ 129
G+AGILRYRGY I LA+++TF EVSYLLI GELPT +L F D IR HTLL ED K
Sbjct: 67 GEAGILRYRGYPIEQLADSSTFIEVSyllIYGELPTQAQLDDFTDIRRHHTLLHEDLKRF 126

Query: 130 FNVFPRDAHPMATLASSVNIILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHRARK 189
F+ FPR+AHPM L+S+VN LS YYQD L+P D Q++ +T+RL+AK+P +AAY+++
Sbjct: 127 FDGFPRNAHPMPVLSSAVNALSAYYQDSLDPDPEQVELSTIRLLAKLPTIAAYSyKKSv 186

Query: 190 GAPYMPDNLNARENFLRMMFGYPTPEYIDPIMVKALDKLLILHADHEQNCSTSTVRM 249
G P++YPDNL ENFLRM FG+P EPYE+DP + ALD LLILHADHEQNCSTSTVR+
Sbjct: 187 GQPFLYPDNLTLVENFLRMTFGFAEPYEVDPVAAALDMLLILHADHEQNCSTSTVRL 246

Query: 250 IGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGV 309
+GS+ AN+F S++GGINAL GPLHGGANQAVLEML+DIK GGD F+ KVKNKEDGV
Sbjct: 247 VGSSDANLFTSVSGGINALWGPLHGGANQAVLEMLDDIK-AQGGDVKEFIRKVKNKEDGV 305

Query: 310 RLMGFGRHRYVKNYDPRAAIVKETAHEILEH-XXXXXXXXXAikLEEIALADDYFISRKLY 368
+LMGFGRHRYV+NYDPRAAI K+ A IL A LEE AL DDYF+ R+LY
Sbjct: 306 KLMGFGRHRYVKNYDPRAAIAKKHADNILRLKLGDDDELFEIAQALEEAALDDYFVERRLY 365

Query: 369 PNVDFTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKES 428
PNVDFTYG+IY+AMGFPT FTVLFA+GRLPGWIAH+RE + + KI RPRQ+YTG +
Sbjct: 366 PNVDFTGVYKAMGFPTRMFTVLFA+GRLPGWIAH+RE-MHSEPLKIGRPRQIYTGyGA 424

Query: 429 R 429

R

Sbjct: 425 R 425

>tr:Q9R339 [Q9R339] Citrate synthase (EC 4.1.3.7). >gpu:SC0939113_211 ▲Top
[AL939113] citrate synthase. [Streptomyces coelicolor
A3(2)]>gp:SC0939113_211 [AL939113] citrate synthase.
[Streptomyces coelicolor A3(2)]>gp:AF181118_1 [AF181118]
citrate synthase [Streptomyces coelicolor]
Length = 429

Score = 536 bits (1382), Expect = e-151

Identities = 265/428 (61%), Positives = 327/428 (76%), Gaps = 2/428 (0%)

Query: 11 NNKAVLHYPGGEFEMDIIEASEGNGVVLGKMLSETGLITFDPGYVSTGSTESKITYIDG 70
+N VL Y GE+ +I+++ G+ G +GK+ ++TGL+T D GY +T + +S ITY+DG
Sbjct: 3 DNSVVLRYGDGEYTPVIDSTVGDKGFDIGKLRAQTGLVTLDSGYGNTAAYKSAITYLDG 62

Query: 71 DAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDFKSQF 130
+AGILRYRGY I LAE ++F EV+YLLINGELPT DEL F EI HTLL ED K+ +
Sbjct: 63 EAGILRYRGYP IEQLAERSSFVEVAYLLINGELPTVDELSAFKGEITQHTLLHEDVKNFY 122

Query: 131 NVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHRARKG 190
FPRDAHPMA L+S V+ LST+YQD NP DE Q + +T+RL+AK+P +AAYA++ G
Sbjct: 123 KGFPRAHPMAMLSVVSALSTFYQDSHNPFDERQRLSTIRLLAKLPTIAAYAYKKSIG 182

Query: 191 APYMPDNLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTSTVRMI 250
P++YP N+L ENFLRM F P + YE+DP +V ALDKLLILHADHEQNCSTSTVR++
Sbjct: 183 HPFVYPANNLGYVENFLRMTFSVPAQEYELDPTVVAALDKLLILHADHEQNCSTSTVRLV 242

Query: 251 GSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGVR 310
GS+QANMF SI+ GINAL GPLHGGANQ+VLEMLE I+ + GGD +F+ KVKNKEDGVR
Sbjct: 243 GSSQANMFASISAGINALWGPLHGGANQSVLEMLEGIR-DAGGDVDSFIRKVKNKEDGVR 301

Query: 311 LMGFGHRVYKKNYDPRAAIVKETAHEILEH-XXXXXXXXXA I KLEEIALADDYFISRKLYP 369
LMGFGHRVYKN+DPRA I+K AH++L A+KLEE AL+DDYF+SR LYP
Sbjct: 302 LMGFGHRVYKNFDPRAK I KAAAHVDLSALGKSDLELDIALKLEEHALSDDYFVSRLYP 361

Query: 370 NVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKESR 429
NVDFYTGLIYRAMGFPT+ FTVLFA+GRLPGWIA + E + G++I RPRQ+YTG R
Sbjct: 362 NVDFYTGLIYRAMGFPTMFVLFALGRLPGWIAQWHEMIKEPGSRIGRPRQIYTGVER 421

Query: 430 KLVPREER 437
VP EER
Sbjct: 422 DFVPVEER 429

>tr:Q7U122 [Q7U122] PROBABLE CITRATE SYNTHASE I GLTA2 (EC
2.3.3.1).>gp:BX248337_9 [BX248337] PROBABLE CITRATE
SYNTHASE I GLTA2 [Mycobacterium bovis AF2122/97]
Length = 431

▲ Top

Score = 535 bits (1377), Expect = e-150
Identities = 264/432 (61%), Positives = 326/432 (75%), Gaps = 2/432 (0%)

Query: 7 VATDNNAKAVLHYPGGFEMDI IEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
+A ++ A L YPGGE ++ I+ A+EG +G+ LG +L++TG TFD G+ +T + +S IT
Sbjct: 1 MADTDDTATLRYPGGEIDLQIVHATEGADGIALGPLLAKTGHTTFDVG FANTAAKSSIT 60

Query: 67 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDF 126
YIDGDAGILRYRGY I LAE +TF EV YLLI GELP D+L +F I+ HT+L ED
Sbjct: 61 YIDGDAGILRYRGYPIDQLAEKSTFIEVCYLLIYGELPDTDQLAQFTGRIQRHTMLHEDL 120

Query: 127 KSQFNVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHR 186
K F+ FPR+AHPM L+S VN LS YYQD L+P+D Q++ +T+RL+AK+P +AAYA++
Sbjct: 121 KRFFDGFPRNAHPMPVLSSVVALSAYYQDALDPMNGQVELSTIRLLAKLPTIAAYAYK 180

Query: 187 ARKGAPYMPDNLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
G P++YPDNSL ENFLR+ FG+P EPY+ DP +V+ALD L ILHADHEQNCSTST
Sbjct: 181 KSVGQPFLLYPDNSLTLVENFLRLTFGFPAPYQADPEVVRALDMLFILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKE 306
VR++GS++AN+F SI+GGINAL GPLHGGANQAVLEMLE I+++ G D + F+ KVKN+E
Sbjct: 241 VRLVGSSRANLFTSISGINALWGPLHGGANQAVLEMLEGIRDS-GDDVSEFVRKVKNRE 299

Query: 307 DGVRLMGFGHRVYKKNYDPRAAIVKETAHEILEHXXXXXXXXXA I KLEEIALADDYFISR 365
GV+LMGFGHRVYKKNYDPRA IVKE A +IL K LEE AL DDYFI R
Sbjct: 300 AGVKLMGFGHRVYKKNYDPRAIRIVKEQADKILAKLGGDSLLGIAKELEEAALDDYFIER 359

Query: 366 KLYPNVDFYTGLIYRAMGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTG 425
KLYPNVDFYTGLIYRA+GFPT FTVLFA+GRLPGWIAH+RE +KI RPRQ+YTG
Sbjct: 360 KLYPNVDFYTGLIYRALGFPTRMFTVLFALGRLPGWIAHWREMHDEGDSKIGRPRQIYTG 419

Query: 426 KESRKLVPREER 437
R V + R
Sbjct: 420 YAERDYVTIDAR 431

>sp:GISY_MYCTU [Q10530] Citrate synthase 1 (EC 2.3.3.1).>pir:E70782 [E70782] [▲Top](#)
probable gltA2 protein - Mycobacterium tuberculosis
(strain H37RV)>gp:AE000516_946 [AE000516] citrate
synthase [Mycobacterium tuberculosis
CDC1551]>gp:BX842574_319 [BX842574] PROBABLE CITRATE
SYNTHASE I GLTA2 [Mycobacterium tuberculosis H37Rv]
Length = 431

Score = 535 bits (1377), Expect = e-150
Identities = 264/432 (61%), Positives = 326/432 (75%), Gaps = 2/432 (0%)

Query: 7 VATDNNAVLHYPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT 66
+A ++ A L YPGGE ++ I+ A+EG +G+ LG +L++TG TFD G+ +T + +S IT
Sbjct: 1 MADTDDTATLRYPGGEIDLQIVHATEGADGIALGPLLAKTGHTTFDVG FANTAAKSSIT 60

Query: 67 YIDGDAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDF 126
YIDGDAGILRYRGY I LAE +TF EV YLLI GELP D+L +F I+ HT+L ED
Sbjct: 61 YIDGDAGILRYRGYPIDQLAEKSTFIEVCYLLIYGELPDTDQLAQFTGRIQRHTMLHEDL 120

Query: 127 KSQFNVFPRDAHPMATLASSVNIILSTYYQDQLNPLDEAQLDKATVRLMAKVPMLAAYHR 186
K F+ FPR+AHPM L+S VN LS YYQD L+P+D Q++ +T+RL+AK+P +AAYA++
Sbjct: 121 KRFFDGFPRNAHPMPVLSSVNVNALSAYYQDALDPMNGQVELSTIRLLAKLPTIAAYAYK 180

Query: 187 ARKGAPYMPDNSLNARENFLRMMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTST 246
G P++YPDNSL ENFLR+ FG+P EPY+ DP +V+ALD L ILHADHEQNCSTST
Sbjct: 181 KSVGQPFYPDNSLTLVENFLRLTFGFPAEPYQADPEVVRALDMLFILHADHEQNCSTST 240

Query: 247 VRMIGSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKE 306
VR++GS++AN+F SI+GGINAL GPLHGGANQAVLEMLE I+++ G D + F+ KVKN+E
Sbjct: 241 VRLVGSSRANLFTSISGGINALWGPLHGGANQAVLEMLEGIRDS-GDDVSEFVRKVKNRE 299

Query: 307 DGVRLMGFGHRVYKNDPRAAIVKETAHEILEHXXXXXXXXXA I K-LEEIALADDYFISR 365
GV+LMGFGHRVYKNDPRA IVKE A +IL K LEE AL DDYFI R
Sbjct: 300 AGVKLMGFGHRVYKNDPRARIVKEQADKILAKLGGDDSLGLIAKELEEAALTDYFIER 359

Query: 366 KLYPNVDFYTG LIYRANGFPTDFFTVLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTG 425
KLYPNVDFYTG LIYRA+GFPT FTVLFA+GRLPGWIAH+RE +KI RPRQ+YTG
Sbjct: 360 KLYPNVDFYTG LIYRALGFPTRMFTVLFALGRLPGWIAHREMHEGDSKIGRPRQIYTG 419

Query: 426 KESRKLVPREER 437
R V + R
Sbjct: 420 YTERDYVTIDAR 431

>tr:Q82CL5 [Q82CL5] Putative citrate synthase.>gpu:BA000030_5334 [BA000030] [▲Top](#)
putative citrate synthase [Streptomyces avermitilis
MA-4680]>gp:AP005042_136 [AP005042] putative citrate
synthase [Streptomyces avermitilis MA-4680]
Length = 429

Score = 533 bits (1372), Expect = e-150
Identities = 262/428 (61%), Positives = 325/428 (75%), Gaps = 2/428 (0%)

Query: 11 NNKAVLHYPGGEFEMDIIEASEGNNGVVLGKMLSETGLITFDPGYVSTGSTESKIT YIDG 70
+N VL Y GE+ +I+++ G+ G +GK+ ++TGL+T D GY +T + +S ITY+DG
Sbjct: 3 DNSVVLRYGDGEYTYPVIDSTVGDKGFDIGKLRAGTGLVTLDSGYGNATAAYKSAITYLDG 62

Query: 71 DAGILRYRGYDIADLAENATFNEVSYLLINGELPTDELHKFNDEIRHHTLLDEDFKSQF 130

+ GILRYRGY I LAE +TF EV+YLLINGELPT DEL F EI HTLL ED K+ +
Sbjct: 63 EQGILRYRGYP I EQLAERSTFLEVAYLL INGELPTVDELSTFKGEITQHTLLHEDVKNFY 122

Query: 131 NVFPRDAHPMATLASSVNI LSTYYQDQLNPLDEAQLDKATVRLMAKVPM LAAYHRARKG 190
FPRDAHPMA L+S V+ LST+YQD NP DE Q + +T+RL+AK+P +AAYA++ G
Sbjct: 123 RGFPRAHPMAM LSSVVSALSTFYQDSHNP FDEKQRLSTIRLLAKLPTIAAYAYKKSIG 182

Query: 191 APYMPDNLNARENFLRMFGYPTEPYEIDPIMVKALDKLLILHADHEQNCSTSTVRMI 250
P++YP N L ENFLRM F P + Y++DP++V ALDKLLILHADHEQNCSTSTVR++
Sbjct: 183 HPFVYPRNDLGYVENFLRM TFSVPAQDYDLDPVVVSALDKLLILHADHEQNCSTSTVRLV 242

Query: 251 GSAQANMFVSIAGGINALSGPLHGGANQAVLEMLEDIKNNHGGDATAFMNKVKNKEDGVR 310
GS+QANMF SI+ GI+AL GPLHGGANQ+VLEMLE I+ + GGD F+ KVKNKEDGV+
Sbjct: 243 GSSQANMFASISAGISALWGPLHGGANQSVLEMLEGIQTS-GGDVDTFIRKVKNKEDGVK 301

Query: 311 LMFGHRVYKNDPRAAIVKETAHEILEH-XXXXXXXXXA I KLEEIALADDYFISRKLYP 369
LMFGHRVYKN+DPRA I+K AH++L A+KLEE ALADDYF+ RKLYP
Sbjct: 302 LMFGHRVYKNFDPRAKI I KAAAHVLSALGKSDEL LDI ALKLEEHALADDYFVERKLYP 361

Query: 370 NVDFYTGLIYRAMGFPTDFFTFLFAIGRLPGWIAHYREQLGAAGNKINRPRQVYTGKESR 429
NVDFYTGLIYRAMGFPT+ FTVLFA+GRLPGWIA + E + G++I RPRQ+YTG+ R
Sbjct: 362 NVDFYTGLIYRAMGFPTMFTVLFAIGRLPGWIAQWHEMIKEPGSRI GRPRQIYTG EVLR 421

Query: 430 KLVPREER 437
VP E R
Sbjct: 422 DFVPVEGR 429

Database: nr-aa: Non-redundant protein sequence database Release
05-01-04

Posted date: Jan 4, 2005 3:40 PM

Number of letters in database: 600,567,511

Number of sequences in database: 1,848,798

Lambda	K	H
0.319	0.137	0.399

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 527,441,587

Number of Sequences: 1848798

Number of extensions: 22621601

Number of successful extensions: 50691

Number of sequences better than 10.0: 10

Number of HSP's better than 10.0 without gapping: 665

Number of HSP's successfully gapped in prelim test: 43

Number of HSP's that attempted gapping in prelim test: 48255

Number of HSP's gapped (non-prelim): 739

length of query: 437

length of database: 600,567,511

effective HSP length: 128

effective length of query: 309

effective length of database: 363,921,367

effective search space: 112451702403

effective search space used: 112451702403

T: 11

A: 40

X1: 16 (7.4 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.7 bits)

S2: 75 (33.5 bits)

=